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<110> Mayfield, Stephen

<120> RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR
EXPRESSION OF RECOMBINANT MOLECULES

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<140> 09/341,550

<141> 1999-07-13

<150> PCT/US98/00840

<151> 1998-01-16

<150> 60/035,955

<151> 1997-01-17

<150> 60/069,400

<151> 1997-12-12

<160> 14

<170> PatentIn Ver. 2.1

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<213> Chlamydomonas reinhardtii

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ctg tcc tgc aag gtt gcc act gac gcc aac ggc gtg tgc aag ggc tac	664
Leu Ser Cys Lys Val Ala Thr Asp Ala Asn Gly Val Ser Lys Gly Tyr	
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acc gtc aac cag aag aag att gag ggc aag atc gtg tac gtg gcc ccc	760
Thr Val Asn Gln Lys Lys Ile Glu Gly Lys Ile Val Tyr Val Ala Pro	
175 180 185	
ttc cag aag cgc gct gac cgc ccc agg gca agg acg ttg tac acc aac	808
Phe Gln Lys Arg Ala Asp Arg Pro Arg Ala Arg Thr Leu Tyr Thr Asn	
190 195 200	
gtg ttc gtc aag aac ttg ccg gcc gac atc ggc gac gac gag ctg ggc	856
Val Phe Val Lys Asn Leu Pro Ala Asp Ile Gly Asp Asp Glu Leu Gly	
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Lys Met Ala Thr Glu His Gly Glu Ile Thr Ser Ala Val Val Met Lys	
225 230 235	
gac gac aag ggc ggc agc aag ggc ttc ggc ttc atc aac ttc aag gac	952
Asp Asp Lys Gly Gly Ser Lys Gly Phe Gly Phe Ile Asn Phe Lys Asp	
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Ala Glu Ser Ala Ala Lys Cys Val Glu Tyr Leu Asn Glu Arg Glu Met	
255 260 265	
agc ggc aag acc ctg tac gcc ggc cgc gcc cag aag aag acc gag cgc	1048
Ser Gly Lys Thr Leu Tyr Ala Gly Arg Ala Gln Lys Lys Thr Glu Arg	
270 275 280	
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Glu Ala Met Leu Arg Gln Lys Ala Glu Glu Ser Lys Gln Glu Arg Tyr	
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Asn Met Gln Ala Arg Met Gly Met Gly Ala Met Ser Arg Pro Pro Asn	
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575 580 585	
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 Asp Glu Ala Ile Ala Val Leu Lys Gln His Asn Val Ile Ala Glu Glu
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 Asn Lys Ala

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 15 20 25

tcc gat gag tat gag gac gac gag gag gac gat gcc ccc gcc gcc cct 147
 Ser Asp Glu Tyr Glu Asp Asp Glu Glu Asp Asp Ala Pro Ala Ala Pro
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 Lys Asp Asp Asp Val Asp Val Thr Val Val Thr Val Lys Asn Trp Asp
 45 50 55 60

gag acc gtc aag aag tcc aag ttc gcg ctt gtg gag ttc tac gct cct 243
 Glu Thr Val Lys Lys Ser Lys Phe Ala Leu Val Glu Phe Tyr Ala Pro
 65 70 75

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 Trp Cys Gly His Cys Lys Thr Leu Lys Pro Glu Tyr Ala Lys Ala Ala
 80 85 90

acc gcc ctg aag gct gct gct ccc gat gcc ctt atc gcc aag gtc gac	339
Thr Ala Leu Lys Ala Ala Ala Pro Asp Ala Leu Ile Ala Lys Val Asp	
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Ala Thr Gln Glu Glu Ser Leu Ala Gln Lys Phe Gly Val Gln Gly Tyr	
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Pro Thr Leu Lys Trp Phe Val Asp Gly Glu Leu Ala Ser Asp Tyr Asn	
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Gln Lys Asn Ser Asp Lys Ile Phe Asn Ser Gly Ile Asn Lys Gln Leu	
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Ser Val Ile Ile Ala Lys Met Asp Gly Thr Glu Asn Glu His Pro Glu	
445 450 455 460	
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Ile Glu Val Lys Gly Phe Pro Thr Ile Leu Phe Tyr Pro Ala Gly Ser	
465 470 475	
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Asp Arg Thr Pro Ile Val Phe Glu Gly Gly Asp Arg Ser Leu Lys Ser	
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ctg acc aag ttc atc aag acc aac gcc aag atc ccg tac gag ctg ccc	1539
Leu Thr Lys Phe Ile Lys Thr Asn Ala Lys Ile Pro Tyr Glu Leu Pro	
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Pro Ala Ser Asp Lys Asp Glu Leu	
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gcttgaattt ataaattaaa atatttttac aatattttac ggagaaatta aaactttaaa 240

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1 5 10	
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Trp Ala Arg Phe Cys Glu Trp Ile Thr Ser Thr Glu Asn Arg Leu Tyr	
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Ser Val Phe Ile Ile Ala Phe Ile Ala Ala Pro Pro Val Asp Ile Asp	
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Gly Ile Arg Glu Pro Val Ser Gly Ser Leu Leu Tyr Gly Asn Asn Ile	
65 70 75	
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Tyr Pro Ile Trp Glu Ala Ala Ser Leu Asp Glu Trp Leu Tyr Asn Gly	
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Tyr Met Gly Arg Glu Trp Glu Leu Ser Phe Arg Leu Gly Met Arg Pro	
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Leu Gly Ile Ser Gly Thr Phe Asn Phe Met Ile Val Phe Gln Ala Glu	
175 180 185	
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His Asn Ile Leu Met His Pro Phe His Met Leu Gly Val Ala Gly Val	
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ttc ggt ggt tca tta ttc tca gct atg cac ggt tct tta gtt act tca	914
Phe Gly Gly Ser Leu Phe Ser Ala Met His Gly Ser Leu Val Thr Ser	
210 215 220	
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Ser Leu Ile Arg Glu Thr Thr Glu Asn Glu Ser Ala Asn Glu Gly Tyr	
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Ala Asp Ile Ile Asn Arg Ala Asn Leu Gly Met Glu Val Met His Glu	
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Arg Asn Ala His Asn Phe Pro Leu Asp Leu Ala Ser Thr Asn Ser Ser	
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Ser Asn Asn	
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Ile Glu Gly Arg His Met Ala Thr Thr Glu Ser Ser Ala Pro Ala Ala	
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acc acc cag ccg gcc agc acc ccg ctg gcg aac tcg tcg ctg tac gtc	144
Thr Thr Gln Pro Ala Ser Thr Pro Leu Ala Asn Ser Ser Leu Tyr Val	
35 40 45	

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Gly Asp Leu Glu Lys Asp Val Thr Glu Ala Gln Leu Phe Glu Leu Phe	
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Ser Ser Val Gly Pro Val Ala Ser Ile Arg Val Cys Arg Asp Ala Val	
65 70 75 80	
acg cgc cgc tcg ctg ggc tac gcc tac gtc aac tac aac agc gct ctg	288
Thr Arg Arg Ser Leu Gly Tyr Ala Tyr Val Asn Tyr Asn Ser Ala Leu	
85 90 95	
gac ccc cag gct gct gac cgc gcc atg gag acc ctg aac tac cat gtc	336
Asp Pro Gln Ala Ala Asp Arg Ala Met Glu Thr Leu Asn Tyr His Val	
100 105 110	
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Val Asn Gly Lys Pro Met Arg Ile Met Trp Ser His Arg Asp Pro Ser	
115 120 125	
gcc cgc aag tcg ggc gtc ggc aac atc ttc atc aag aac ctg gac aag	432
Ala Arg Lys Ser Gly Val Gly Asn Ile Phe Ile Lys Asn Leu Asp Lys	
130 135 140	
acc atc gac gcc aag gcc ctg cac gac acc ttc tcg gcc ttc ggc aag	480
Thr Ile Asp Ala Lys Ala Leu His Asp Thr Phe Ser Ala Phe Gly Lys	
145 150 155 160	
att ctg tcc tgc aag gtt gcc act gac gcc aac ggc gtg tcg aag ggc	528
Ile Leu Ser Cys Lys Val Ala Thr Asp Ala Asn Gly Val Ser Lys Gly	
165 170 175	
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Tyr Gly Phe Val His Phe Glu Asp Gln Ala Ala Ala Asp Arg Ala Ile	
180 185 190	
cag acc gtc aac cag aag aag att gag ggc aag atc gtg tac gtg gcc	624
Gln Thr Val Asn Gln Lys Lys Ile Glu Gly Lys Ile Val Tyr Val Ala	
195 200 205	
ccc ttc cag aag cgc gct gac cgc ccc agg gca agg acg ttg tac acc	672
Pro Phe Gln Lys Arg Ala Asp Arg Pro Arg Ala Arg Thr Leu Tyr Thr	
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aac gtg ttc gtc aag aac ttg ccg gcc gac atc ggc gac gac gag ctg	720
Asn Val Phe Val Lys Asn Leu Pro Ala Asp Ile Gly Asp Asp Glu Leu	
225 230 235 240	
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Gly Lys Met Ala Thr Glu His Gly Glu Ile Thr Ser Ala Val Val Met	
245 250 255	
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Lys Asp Asp Lys Gly Gly Ser Lys Gly Phe Gly Phe Ile Asn Phe Lys	
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Asp Ala Glu Ser Ala Ala Lys Cys Val Glu Tyr Leu Asn Glu Arg Glu	
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Met Ser Gly Lys Thr Leu Tyr Ala Gly Arg Ala Gln Lys Lys Thr Glu	
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Arg Glu Ala Met Leu Arg Gln Lys Ala Glu Glu Ser Lys Gln Glu Arg	
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Tyr Leu Lys Tyr Gln Ser Met Asn Leu Tyr Val Lys Asn Leu Ser Asp	
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Thr Ile Thr Ser Cys Lys Val Met Lys Asp Gly Ser Gly Lys Ser Lys	
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Gly Phe Gly Phe Val Cys Phe Thr Ser His Asp Glu Ala Thr Arg Pro	
370 375 380	
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Pro Val Thr Glu Met Asn Gly Lys Met Val Lys Gly Lys Pro Leu Tyr	
385 390 395 400	
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Val Ala Leu Ala Gln Arg Lys Asp Val Arg Arg Ala Thr Gln Leu Glu	
405 410 415	
gcc aac atg cag gcg cgc atg taa gga tcc	1278
Ala Asn Met Gln Ala Arg Met	
420	

B1
Concluded